

RESULT 1  
 PCT-US01-32045-105  
 ; Sequence 105, Application PC/TUS0132045  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Wilson, Keith E.  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: Revezl, Peter  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Prostate Cancer, Compositions  
 ; TITLE OF INVENTION: and Methods of Screening for Modulators of Prostate  
 ; TITLE OF INVENTION: Cancer  
 ; FILE REFERENCES: 018501-004200PC  
 ; CURRENT APPLICATION NUMBER: PCT/US01/32045  
 ; CURRENT FILING DATE: 2002-08-22  
 ; PRIOR APPLICATION NUMBER: US 09/687,576  
 ; PRIOR FILING DATE: 2000-10-13  
 ; PRIOR APPLICATION NUMBER: US 09/733,288  
 ; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: US 09/733,742  
 ; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: US 60/263,957  
 ; PRIOR FILING DATE: 2001-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/276,791  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: US 60/276,888  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: US 60/281,922  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/286,214  
 ; PRIOR FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: US 09/847,046  
 ; PRIOR FILING DATE: 2001-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/288,589  
 ; PRIOR FILING DATE: 2001-05-04  
 ; NUMBER OF SEQ ID NOS: 296  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 105  
 ; LENGTH: 3810  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-32045-105

Alignment Scores:

Pred. No.:	0	Length:	3810
Score:	5888.00	Matches:	1123
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	1	Gaps:	0

US-10-643-795A-123 (1-1127) x PCT-US01-32045-105 (1-3810)

Qy	5 ThrGluLysProThrAspAlaTyrGlyGluLeuAspPheThrGlyAlaGlyArgLysHis 24
Db	3 ACGGAGAACGCCACCGATGCCATCGGAGAGCTGGACTTCACGGGGGGCGCCGCAAGCAC 62
Qy	25 SerAsnPheLeuArgLeuSerAspArgThrAspProAlaAlaValTyrSerLeuValThr 44
Db	63 AGCAAATTCTCCGGCTCTGACCGAACGGATCCAGCTGCAAGTTATAGCTGGTCACA 122
Qy	45 ArgThrTrpGlyPheArgAlaProAsnLeuValSerValLeuGlyGlySerGlyGly 64
Db	123 CGCACATGGGGCTTCCGTGCCCCGAACCTGGTGTGTCAGTGTGCTGGGGGATGGGGGC 182
Qy	65 ProValLeuGlnThrTrpLeuGlnAspLeuLeuArgArgGlyLeuValArgAlaAlaGln 84
Db	183 CCCGCTCCAGACCTGGCTCGAGACCTGCTGGCTGTTGGCTGGTGGCGCTGCCAG 242
Qy	85 SerThrGlyAlaTrpIleValThrGlyGlyLeuHisThrGlyIleGlyArgHisValGly 104

Db 243 AGCACAGGAGCCTGGATGTCACTGGGGTCTGCCACACGGGCATGGCCGGCATGTTGGT 302  
Qy 105 ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrLysValValAlaMetGly 124  
Db 303 GTGCCCTGACGGGACCATCAGATGGCCAGCACTGGGGCACCAAGGTGGTGGCCATGGT 362  
Qy 125 ValAlaProTrpGlyValValArgAsnArgAspThrIleIleAsnProlysGlySerPhe 144  
Db 363 GTGGCCCCCTGGGTGTTGTCGGGAATAGACACACCCCTCATCAACCCCCAAGGGCTCGTC 422  
Qy 145 ProAlaArgTyrArgTrpArgGlyAspProGluAspGlyValGlnPheProIeuAspTyr 164  
Db 423 CCTCCGAGCTTACCGGTGGCGGTTGACCCGGACGGGCTCCAGTTCCCTGGACTAC 482  
Qy 165 AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlyGlyGluAsn 184  
Db 483 AAACTACTGGCCCTCTCTCTGGTGGACGACGGCACACCGCTGGCTGGGGGGCAGAAC 542  
Qy 185 ArgPheArgLeuArgLeuGluSerTyrIleSerGlnGlnLysThrGlyValGlyGlyThr 204  
Db 543 CGCTTCCGGCTTGGCCCTGGACTCTTACATCTCACACAGAGAACGAGCAGGGCTGGAGGACT 602  
Qy 205 GlyIleAspIleProValIleLeuIleAspGlyAspGluLysMetLeuThrArg 224  
Db 603 GGAATTGACATCCCTGTCCTGCTCTCTGATTGATGGTGTAGAAGATGTTGACGCCA 662  
Qy 225 IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla 244  
Db 663 ATAGAGAACGCCACCCAGGGCTCAGCTCCCAATGTCCTCTGCTGGCTGGCTAGGGGAGCT 722  
Qy 245 AlaAspCysLeuAlaGluThrLeuGluAspThrLeuAlaProGlySerGlyGlyAlaArg 264  
Db 723 CGCGACTGCGCTGGGGAGACCTGGAAAGACACTTGGCCCAAGGGAGTGGGGAGCCAGG 782  
Qy 265 GlnGlyGluAlaArgAspArgIleArgArgPhePheProlysGlyAspLeuGluValLeu 284  
Db 783 CAAGGGGAAGCCCGAGATCGAAATCAGGGTTCTTCCAAAGGGGACCTTGAGGTCTG 842  
Qy 285 GlnAlaIleValGluArgIleMetThrArgLysGluIleLeuThrValTyrSerSerGlu 304  
Db 843 CAGGCCAAGGGTGGAGGAGATTATGACCCGGAAGGAGCTCTGACAGTCTATCTCTGAG 902  
Qy 305 AspGlySerGluGluPheGluThrIleValLeuLysAlaIleValLysAlaCysGlySer 324  
Db 903 GATGGGTCTGAGGAATTGGAGACCATAGTTTGAAGGCCCTTGTGAAGGCCCTGGGACG 962  
Qy 325 SerGluAlaSerAlaTyrLeuAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp 344  
Db 963 TCGGAGGCCCTCAGCCTACCTGGATGAGCTGCGTTGGCTGTGGCTTGGAAACCGCTGGAC 1022  
Qy 345 IleAlaIleSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla 364  
Db 1023 ATTCGGGAAAGTGTGAACTCTTCCGGGGGACATCCAAATGGGGCTTCCCATCTGAGGCT 1082  
Qy 365 SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis 384  
Db 1083 TCCCTCATGGACGCCCTGCTGAATGACCCGGCTGGAGTTCTGCGCTTGGCTCATTTCCAC 1142  
Qy 385 GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla 404  
Db 1143 GGCCTCAGGCTGGCCACCTTCCTGACCCCGATGCCCTGGCCCCAACTCTCACAGGGCGGGG 1202  
Qy 405 ProSerAsnSerLeuLeuArgAsnLeuLeuAspGlnAlaSerHisSerAlaGlyThrLys 424  
Db 1203 CCCTCCAACTCCCTCATCCCAACCCATTTCACCAACCCCTCCCCAACCCACCCACCCAAA 1262  
Qy 425 AlaProAlaLeuLysClyClyAlaAlaGluLeuArgProAspValClyHisValLeu 444  
Db 1263 GCCCCAGCCCTAAAGCCCGAGCTCCGGAGCTCCCCCCCCCTGACCTGGGGCATGTGCTG 1322

Qy 445 ArgMetLeuLeuGlyLysMetCysAlaProArgTyrProSerGlyGlyAlaTrpAspPro 464  
 Db 1323 AGGATGCTCTGGGGAGATCTGGCGGCCGAGGTACCCCTCCGGGGGCCCTGGGACCT 1382  
 Qy 465 HisProGlyGlnGlyPheGlyGluSerMetTyrLeuLeuSerAspLysAlaThrSerPro 484  
 Db 1383 CACCCAGGCCAGGCCTTCGGGAGACCATGTATCTGCTCTCGGACAAAGCCACCTGGCC 1442  
 Qy 485 LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTrpSerAspLeuLeuLeuTrpAlaLeu 504  
 Db 1443 CTCTCGCTGGATGCTGGCCCTGGCGAGCCCCCTGGACCGAACCTGCTCTGGGCACTG 1502  
 Qy 505 LeuLeuAsnArgAlaGlnMetAlaMetTyrPheTrpGluMetGlySerAsnAlaValSer 524  
 Db 1503 TTGCTGAAACAGGCKACAGATTCGCAATGTACTCTGGGAAATGGGTTCAAATGCAATTTC 1562  
 Qy 525 SerAlaLeuGlyAlaCysLeuLeuLeuArgValMetAlaArgLeuGluProAspAlaGlu 544  
 Db 1563 TCAGCTCTTGGGCCTGTTCTGCTCCGGGTGATGGCACGCCCTGGACCCCTGAGCTGAG 1622  
 Qy 545 GluAlaAlaArgArgLysAspLeuAlaPheLysPheGluGlyMetGlyValAspLeuPhe 564  
 Db 1623 GAGGCCACCGAGGAAAGCCTGGCTTCAACTTTGAGGGATGGCCGTGACCCCTTT 1682  
 Qy 565 GlyGlycineTyrArgSerSerGluValArgAlaAlaArgLeuLeuLeuArgArgCysPro 584  
 Db 1683 GGGCAGGTGCTATCCGACAGTGAGGTGAGGGCTGCCGCCCTCTCTCCGGCTGGCG 1742  
 Qy 585 LeuTrpGlyAspAlaThrCysLeuGlnLeuAlaMetGlnAlaAspAlaArgAlaPhePhe 604  
 Db 1743 CTCTGGGGGATGCCACTTGCTCTAGCTGGCCATGCAAGCTGAGCCCGTCCCTCTT 1802  
 Qy 605 AlaGlnAspGlyValGlnSerLeuLeuThrGlnLysTrpTrpGlyAspMetAlaSerThr 624  
 Db 1803 GCCCCAGGATGGGGTACAGTCCTGCTGACACAGAACGAGTGGGGAGATATGCCAGCACT 1862  
 Qy 625 ThrProIleTrpAlaLeuValLeuAlaPhePheCysProProIleIleTyrThrArgLeu 644  
 Db 1863 ACACCCATCTGGGCCCTGGTCTCGCCCTCTTGGCCCTCCACTCATCTACACCCGCCCTC 1922  
 Qy 645 IleThrPheArgLysSerGluGluGluProThrArgGluLeuGluPheAspMetAsp 664  
 Db 1923 ATCACCTTCAGGAAATCAGAAAGGAGGCCACACGGAGGGCTAGAGTTGACATGAT 1982  
 Qy 665 SerValIleAsnGlyGlyGlyProValGlyThrAlaAspProAlaGlyLysThrProLeu 684  
 Db 1983 AGTGTCAATTATGGGGAAAGGCCCTGTCGGACCGGGGACCCAGCCGGAGAAAGCAGCGCTG 2042  
 Qy 685 GlyValProArgGlnSerGlyArgProGlyCysGlyArgCysGlyGlyArgArg 704  
 Db 2043 GGGGTCCCAGCCGAGCTGGGCCCTCCGGGTGCTGGGGGGGCCGCTGGGGGGGCCGG 2102  
 Qy 705 CysLeuArgArgTrpPheHisPheTrpGlyAlaProValThrIlePheMetGlyAsnVal 724  
 Db 2103 TGCCCTACGGCGCTGGTCTCACTCTGGGGGCCCGGTGACCATCTTCATGGCAACGIG 2162  
 Qy 725 ValSerTyrLeuLeuPheLeuLeuLeuPheSerArgValLeuLeuValAspPheGlnPro 744  
 Db 2163 GTCACTGACTCTGCTGTTCTGCTCTTCTGGCGGGTGCCTGCTGTTGGGATTTCCAGCGG 2222  
 Qy 745 AlaProProGlySerLeuGluLeuLeuLeuTyrPheTrpAlaPheThrLeuLeuCysGlu 764  
 Db 2223 GCGCCGCCGCGCTCCCTGGAGCTGCTGCTCJATTCTGGCTTTCAGGCTGCTGCGAG 2282  
 Qy 765 GluLeuArgGlnGlyLeuSerGlyGlyGlySerLeuAlaSerGlyGlyProGlyPro 784  
 Db 2283 GAACTGCGCCAGGGCTGAGCGGAGGCCGGGGCACCTCCCGAACGGGGGCCCGGCC 2342  
 Qy 785 GlyHisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAsnGlnCys 804  
 Db 2343 GGGCATGCTCACTGAGGCCAGCCCTGCGCCTTACCTCGCCGACAGCTGGAACAGCTGCC 2402

Qy 805 AspLeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeu 824  
 |||||  
 Db 2403 GACCTAGTCGCTCTCACCTGCTTCCATCGCTGGCGCTGCCGCTGACCCGGGTGG 2462  
  
 Qy 825 TyrHisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuIle 844  
 |||||  
 Db 2463 TACCAACCTGGGCCCACTGTCCCTCTCATCGACTTCATGGTTTTACCGTGGCGCTGCTT 2522  
  
 Qy 845 HisIlePheThrValAsnLysGlnLeuGlyProLysIleValIleValSerLysMetMet 864  
 |||||  
 Db 2523 CACATCTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGACCAAGATGATG 2582  
  
 Qy 865 LysAspValPhePhePheLeuPhePheLeuGlyValIrpLeuValAlaTyrGlyValAla 884  
 |||||  
 Db 2583 AAGGACGTGTTCTCTCTCTCTCTCGGGGTGGCTGCTGCTGATGCTATGGCTTGCCC 2642  
  
 Qy 885 ThrGluGlyLeuLeuArgProArgAspSerAspPheProSerIleLeuArgArgValPhe 904  
 |||||  
 Db 2643 ACGGAGGGCCTCTGAGGCCACGGGACAGTGACTTCCCAAAGTATCTCGGCGCGCTTC 2702  
  
 Qy 905 TyrArgProTyrLeuGlnIlePheGlyGlnIleProGlnGluAspMetAspValAlaLeu 924  
 |||||  
 Db 2703 TACGGTCCCTACCTGAGATCTCGGAGATTCCCAGGAGGACATGGACCTGGCCCT 2762  
  
 Qy 925 MetGluHisSerAsnCysSerSerGluProGlyPheTrpIleHisProProGlyAlaGln 944  
 |||||  
 Db 2763 ATGGAGCACAGCAACTGCTCGGAGGCCGCTCTGGCACACCCCTCTGGGGCCAG 2822  
  
 Qy 945 AlaGlyThrCysValSerGlnTyrAlaAsnTrpLeuValIleLeuLeuValIlePhe 964  
 |||||  
 Db 2823 GGGGGCACCTCGCTCTCCCACTATGCCAACCTGGCTGGTGGCTGCTCTCGTCATCTTC 2882  
  
 Qy 965 LeuLeuValAlaAsnIleLeuleuValAsnLeuLeuIleAlaMetPheSerTyrThrPhe 984  
 |||||  
 Db 2883 CTGGCTGGGCCAACATCTCGCTGGTCAACITGCTCATGGCATATGGCATTTACACATT 2942  
  
 Qy 985 GlyLysValGlnGlyAsnSerAspLeuIleTrpLysAlaGlnArgTyrArgLeuIleArg 1004  
 |||||  
 Db 2943 GCGAAAGTCAGGCCAACGGCATCTACTGGAAAGGGCACCGGTACCGCCCTCATCCGG 3002  
  
 Qy 1005 GluPheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgLeu 1024  
 |||||  
 Db 3002 GAATTCACCTCTCGGCCCCCGCTGGCCCCGCCCTTATCGTCATCTCCACATGGCCTC 3062  
  
 Qy 1025 LeuLeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlu 1044  
 |||||  
 Db 3063 CTGGCTCAGGCCAATTTGTCAGGCCAACCGGGGAGCCCCCACGGCTCTCCCCGGCCCTGGAG 3122  
  
 Qy 1045 HisPheArgValTyrLeuSerLysGluAlaGluArgLysLeuLeuThrTrpGluSerVal 1064  
 |||||  
 Db 3123 CATTTCGGGTTTACCTTCTAAAGGAAAGCCGAGCGGAAGCTGCTAACGTGGAAATCGGTG 3182  
  
 Qy 1065 HisLysGluAsnPheLeuLeuAlaArgAlaArgAspLysArgGluSerAspSerGluArg 1084  
 |||||  
 Db 3183 CATAAAGGAGAACCTTCTGCTGGCACGCCCTAGGGGACAAGGGGGAGGCCGACTCCGAGCGT 3242  
  
 Qy 1085 LeuGluArgThrSerGlnLysValAspLeuAlaLeuLysGlnLeuGlyHisIleArgGlu 1104  
 |||||  
 Db 3243 CTGGAGGGCACGTCGGCAAGGTGGACTTGCCACTGAAACAGCTGGACACATCCGGAG 3302  
  
 Qy 1105 TyrGluGlnArgLeuLysValLeuGluArgGluValGlnGlnCysSerArgValLeuGly 1124  
 |||||  
 Db 3303 TACGAACAGCGCCTGAAAGTGTCTGGAGCGGGAGGTCAGCTGAGTGTAGCCGCTCTGGGG 3362  
  
 Qy 1125 ItpValIthr 1127  
 |||||  
 Db 3363 TGGGTGACG 3371

RESULT 2  
 US-09-976-858-105

; Sequence 105, Application US/09976858  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Wilson, Keith E.  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: Peter, Kerevi  
 ; TITLE OF INVENTION: Methods of Diagnosis of Prostate Cancer, Compositions and Methods  
 ; TITLE OF INVENTION: of Screening for Modulators of Prostate Cancer  
 ; FILE REFERENCE: 05882,0183.NPUS00  
 ; CURRENT APPLICATION NUMBER: US/09/976,858  
 ; CURRENT FILING DATE: 2001-10-12  
 ; PRIOR APPLICATION NUMBER: 60/276,791  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/288,589  
 ; PRIOR FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: 60/276,888  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/286,214  
 ; PRIOR FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: 60/281,922  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/263,957  
 ; PRIOR FILING DATE: 2001-01-24  
 ; NUMBER OF SEQ ID NOS: 294  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 105  
 ; LENGTH: 3810  
 ; TYPE: DNA  
 ; ORGANISM: human organism  
 US-09-976-858-105

Alignment Scores:

Pred. No.:	0	Length:	3810
Score:	5888.00	Matches:	1123
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	37	Gaps:	0

US-10-643-795A-123 (1-1127) x US-09-976-858-105 (1-3810)

Qy	5 ThrGluLysProThrAspAlaTyrGlyGluLeuAspPheThrGlyAlaGlyArgLysHis 24
Db	3 ACGGAGAACCCACCGATGCCCTACGGAGAGCTGGACCTCACGGGGGCCGGCAAGCAC 62
Qy	25 SerAsnPheLeuArgLeuSerAspArgThrAspProAlaAlaValTyrSerLeuValThr 44
Db	63 AGCAAATTCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGCTGGTCACA 122
Qy	45 ArgThrTrpGlyPheArgAlaProAsnLeuValValSerValleuGlyGlySerGlyGly 64
Db	123 CGCACATGGGGCTCCGTCGCCCCAACCTGGTGTGTCAGTCCTGGGGGATCGGGGGC 182
Qy	65 ProValleuGlnThrTrpLeuGlnAspLeuLeuArgArgGlyLeuValArgAlaAlaGln 84
Db	183 CCCGCTCTCAGACCTGGCTCGAGACCTGCTGGCTGTGGCTGGCGGCTGCCCAG 242
Qy	85 SerThrGlyAlaTrpLeuValThrGlyGlyLeuHisThrGlyIleGlyArgHisValGly 104
Db	243 AGCACAGGACCTGGATTGTCACCTGGGGCTCGCACACGGGCATCGGCCGGCATGGTGGT 302
Qy	105 ValAlaValArgAspHisGlnMetAlaSerThrGlyGlyThrLysValValAlaMetGly 124
Db	303 GTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGCACCAAGGTGGTGGCCATGGGT 362
Qy	125 ValAlaProTrpGlyValValArgAsnArgAspThrIleAsnProLysGlySerPhe 144
Db	363 GTGGCCCGCTGGGGTGTGGTCGGGAATAGAGACACCCATCAACCCCCAAGGGCTCGTTC 422
Qy	145 ProAlaArgTyrArgTrpArgGlyAspProGluAspGlyValGlnPheProLeuAspTyr 164

Db 423 CCTCCGGAGGTACCGGTGGCGGGTGACCCGGAGGACGGGTCCAGTTTCCCTGGACTAC 482  
Qy 165 AsnTyrSerAlaPhePheLeuValAspAspGlyThrHisGlyCysLeuGlyGlyGluAsn 184  
Db 483 AACTACTCGGCCCTCTCCCTCGTGGACGACGCCACACCGGTGCGCTGGGGCCGGAGAAC 542  
Qy 185 ArgPheArgLeuArgLeuGluSerTyrIleSerGlnGlnIleThrGlyValGlyGlyThr 204  
Db 543 CGCTTCCCGCTTGGCCCTGGACTCTTACATCTCACACAGAACACCGGCCGTCGGAGCGACT 602  
Qy 205 GlyIleAspIleProValIleLeuLeuIleAspGlyAspGluLysMetLeuThrArg 224  
Db 603 GGAATTCGACATCCCTGTCTCTCTCTGATTGATCGTATGAAACATGTCGACCGGA 662  
Qy 225 IleGluAsnAlaThrGlnAlaGlnLeuProCysLeuLeuValAlaGlySerGlyGlyAla 244  
Db 663 ATAGAGAACGCCACCCAGGCTCACTCTCCATGTCCTCTGCTGGCTGGCTACGGGGAGCT 722  
Qy 245 AlaAspCysLeuAlaGluThrLeuGluAspThrLeuAlaProGlySerGlyGlyAlaArg 264  
Db 723 GCGGACTTGCCCTGGGGAGACCTGGAAAGACACTCTGGCCCAAGGGAGTGGGGAGCCAGG 782  
Qy 265 GlnGlyGluAlaArgAspArgIleArgArgPhePheProLysGlyAspLeuGluValLeu 284  
Db 783 CAAGGCGAAGCCCAGATCGAATCAGCGTITCTTCCAAAGGGGACCTTGAGGTCTG 842  
Qy 285 GlnAlaGlnValGluArgIleMetThrArgLysGluLeuLeuThrValTyrSerSerGlu 304  
Db 843 CAGGCCCAAGGTGGAGGAGATTATGACCCGGAAAGGAGCTCCGACAGTCTATTCCTGAG 902  
Qy 305 AspGlySerGluGluPheGluThrIleValLeuLysAlaLeuValLysAlaCysGlySer 324  
Db 903 GATGGGCTGAGGAATTGGACGACCAIAGTTTGAAGGCCCTGTGAAGGCCCTGTGGGAGC 962  
Qy 325 SerGluAlaSerAlaTyrLeuAspGluLeuArgLeuAlaValAlaTrpAsnArgValAsp 344  
Db 963 TCGGAGGCCCTCAGCCTACCTGGATGAGCTGCGTTGGCTTGGCTTGGAAACCGCGTGGAC 1022  
Qy 345 IleAlaGlnSerGluLeuPheArgGlyAspIleGlnTrpArgSerPheHisLeuGluAla 364  
Db 1023 ATTCGGCAAGACTGAACTCTTGGGGGGGACATCCAAATGGGGTCTTCCATCTGAAAGCT 1082  
Qy 365 SerLeuMetAspAlaLeuLeuAsnAspArgProGluPheValArgLeuLeuIleSerHis 384  
Db 1083 TCCCTCATGACGCCCTGCTGAATGACCGGCCCTGAGCTGCGCTTGGCTTGGCTTGGAC 1142  
Qy 385 GlyLeuSerLeuGlyHisPheLeuThrProMetArgLeuAlaGlnLeuTyrSerAlaAla 404  
Db 1143 GGCCCTAGCCCTGGCCACTTCTGACCCGATGCCCTGGCCCAACTCTACAGCGCGCG 1202  
Qy 405 ProSerAsnSerLeuIleArgAsnLeuLeuAspGlnAlaSerHisAlaGlyThrLys 424  
Db 1203 CCCTCCAACTCGCTCATCGCCACCTTTGGACCAAGGGGTCCCACAGGGAGGACCCAA 1262  
Qy 425 AlaProAlaLeuLysGlyGlyAlaAlaGluLeuArgProProAspValGlyHisValLeu 444  
Db 1263 GCCCCAGCCCTAAAGGGGGAGCTGGGGAGCTCCGGGCCCTGACGTGGGGCATGTCCTG 1322  
Qy 445 ArgMetLeuLeuGlyLysMetCysAlaProArgTyrProSerGlyGlyAlaTrpAspPro 464  
Db 1323 AGGATGCTCTGGGGAAAGATGTCGCGGCCGAGGTACCCCTCCGGGGGCCCTGGGACCT 1382  
Qy 465 HisProGlnGlyPheGluSerMetTyrLeuLeuSerAspLysAlaThrSerPro 484  
Db 1383 CACCCAGGGCAGGCCCTCGGGAGAGCATGATCTGCTCTCGGACAGGCCACCTGGCC 1442  
Qy 485 LeuSerLeuAspAlaGlyLeuGlyGlnAlaProTrpSerAspLeuLeuTrpAlaLeu 504  
Db 1443 CTCTCGCTGGATGCTGGCTCGGGCAGGGCCCTGGAGGCCACCTGCTTGGGCACCTG 1502

Qy 505 LeuLeuAsnArgAlaGlnMetAlaMetTyrPheTrpGluMetGlySerAsnAlaValSer 524  
 |||||  
 Db 1503 TTGCTGAAACAGGGCACAGATGGGCAATGTACTCTGGAGATGGGTTCAAATGCACTTTC 1562  
 Qy 525 SerAlaLeuGlyAlaCysLeuLeuLeuArgValMetAlaArgLeuGluProAspAlaGlu 544  
 |||||  
 Db 1563 TCAGCCTTGGGCCIGITTCCTGCTCCGGGTGATGCCACGCCCTGACCCCTGACCCCTGAG 1622  
 Qy 545 GluAlaAlaArgArgLysAspLeuAlaPheLysPheGluGlyMetGlyValAspLeuPhe 564  
 |||||  
 Db 1623 GAGGCASCAGGAGAAGACCTGGCCTCAAGTTTGAGGGATGGCGTIGACCCCTT 1682  
 Qy 565 GlyGluCysTyrArgSerSerGluValArgAlaAlaArgLeuLeuLeuArgArgCysPro 584  
 |||||  
 Db 1683 GCGGAGCTCTATCCAGACAGTGAGCTGAGGGCTGCCCGCTCTCCCTCCGTCGCTGCCUG 1742  
 Qy 585 LeuTrpGlyAspAlaThrCysLeuGlnLeuAlaMetGlnAlaAspAlaArgAlaPhePhe 604  
 |||||  
 Db 1743 CTCCTGGGGGAGATGCCACTTGGCTTCAGCTGGCCATGCAACCTGACGCCCGTCCCTCTT 1802  
 Qy 605 AlaGlnAspGlyValGlnSerLeuLeuThrGlnLysTrpTrpGlyAspMetAlaSerThr 624  
 |||||  
 Db 1803 GCGCAGGAATGGGGTACAGTCCTGCTGACACAGAAGTGGGGAGATATGCCAGCACT 1862  
 Qy 625 ThrProIleTrpAlaLeuValLeuAlaPhePheCysProProLeuIleTyrThrArgLeu 644  
 |||||  
 Db 1863 ACACCCATCTGGGCCCTGGTCTCGCCCTCTTCCCTCACTGATCTACACCCGCCCTC 1922  
 Qy 645 IleThrPheArgLysSerGluGluGluProThrArgGluGluLeuGluPheAspMetAsp 664  
 |||||  
 Db 1923 ATCACCTTCAGGAAATCAGAAAGAGGAGGCCAACCGGAGGAGCTAGAGTTGACATGAT 1982  
 Qy 665 SerValIleAsnGlyGluGlyProValGlyThrAlaAspProAlaGluLysThrProLeu 684  
 |||||  
 Db 1983 AGTGTCTTAAATGGGAAGGGCCCTGCGGACGGGGGACCCAGCCGAGAAAGACCCCGCTG 2042  
 Qy 685 GlyValProArgGlnSerGlyArgProGlyCysCysGlyArgCysGlyGlyArgArg 704  
 |||||  
 Db 2043 GGGGTCCCAGCCAGTCGGCCGTCGGGGTTGCTCGGGGGGCCGCTCGGGGGGGCCCG 2102  
 Qy 705 CysLeuArgArgTrpPheHisPheTrpGlyAlaProValThrIlePheMetGlyAsnVal 724  
 |||||  
 Db 2103 TGCCTACGCCGCTGGTCTCACTCTGCGGCGCCCGGTGACCATCTTCATGGCACCGTG 2162  
 Qy 725 ValSerTyrLeuLeuPheLeuLeuLeuPheSerArgValLeuLeuValAspPheGlnPro 744  
 |||||  
 Db 2163 GTCACTTACCTGCTGTCCTGCTGCTCTTCCTGGCGGTGCTGCTGTTCCAGCCCG 2222  
 Qy 745 AlaProProGlySerLeuGluLeuLeuLeuTyrPheTrpAlaPheThrLeuLeuCysGlu 764  
 |||||  
 Db 2223 GCGCCGCCGCCGCTCCCTGGAGCTGCTGCTCTATTCCTGGCTTACCGCTGCTGCGAG 2282  
 Qy 765 GluLeuArgGlnGlyLeuSerGlyGlyGlyGlySerLeuAlaSerGlyGlyProGlyPro 784  
 |||||  
 Db 2283 GAACTGGCGCAGGCCCTGAGCGGAGGGCGGGGACCCCTGCCAGGGGGGCCCGGCC 2342  
 Qy 785 GlyHisAlaSerLeuSerGlnArgLeuArgLeuTyrLeuAlaAspSerTrpAsnGlnCys 804  
 |||||  
 Db 2343 GGCCTACCTCACTGAGCCACGCCCTGGGCCCTACCTGCCCGACAGCTGGACCCAGTC 2402  
 Qy 805 AspLeuValAlaLeuThrCysPheLeuLeuGlyValGlyCysArgLeuThrProGlyLeu 824  
 |||||  
 Db 2403 GACCTATGGCTCTCACCTGCTTCTCTCTGGCGTGGGCTGCCGCTGACCCGGGTTG 2462  
 Qy 825 TyrHisLeuGlyArgThrValLeuCysIleAspPheMetValPheThrValArgLeuLeu 844  
 |||||  
 Db 2463 TACCAACTGGGCCGACTGTCTGCACTTCACTGTTTACCGTGGCTGCGCTGCT 2522  
 Qy 845 HisIlePheThrValAsnLysGlnLeuGlyProLysIleValLeuValSerLysMetMet 864  
 |||||  
 Db 2523 CACATCTCACGCTCAACAAAAGCTGGGCCCAAGATCGTCATCGTGAGCAAGATGATG 2582

Qy	865	LysAspValPhePheLeuPheLeuValIleGlyValIleLeuValAlaTyrGlyValAla	884
Db	2583	AAGGACGTGTCCTCTTCCCTCTTCCCTCGGCCGTGGCTGGCTAGCTATGGCTGGCC	2642
Qy	885	ThrGluGlyLeuIleArgProArgAspSerAspPheProSerIleLeuArgArgValPhe	904
Db	2643	ACGGAGGGCTCCCTAGGGCAACGGGACAGTCACTCCAACTATCTCCGGCCGCTTC	2702
Qy	905	TyrArgProTyrLeuGlnIlePheGlyGlnIleProGlnGluAspMetAspValAlaIle	924
Db	2703	TACCGTCCCTAACCTCCAGATCTCGGGCAGATTCCTCCAGAGGACATCGACGTGGCCCTC	2762
Qy	925	MetGluHisSerAsnCysSerSerGluProGlyPheTrpAlaHisProProGlyAlaGln	944
Db	2763	ATGGAGCACGCAACTCTCGTCGGAAGCCCGCTCTGGCAACACCTCTCGGGCCCAAG	2822
Qy	945	AlaGlyThrCysValSerGlnTyrAlaAsnTrpLeuValValLeuLeuValIlePhe	964
Db	2823	GGCGGCCACTCGGGCTCCCTAGCCAACTGCACTTGCTGGCTGCTCTCGTCATCTTC	2882
Qy	965	LeuLeuValAlaAsnIleLeuLeuValAsnLeuLeuIleAlaMetPheSerTyrThrPhe	984
Db	2883	CTGCTCGTGGCCAACATCTGCTGGTCACTTGCTATTGCCATGTCAGTTACACATT	2942
Qy	985	GlyLysValGlnIleAsnSerAspLeuTyrTrpIleAlaGlnArgTyrArgLeuIleArg	1004
Db	2943	GGCAAAGTACAGGGAAACAGCGCATCTCTACTGGAAAGGGCCAGCGTTACCGCTCATCGG	3002
Qy	1005	GluPheHisSerArgProAlaLeuAlaProProPheIleValIleSerHisLeuArgleu	1024
Db	3003	GAATTCACCTCGCCCGCGCTGGCCCGGCCCTTATGCTCATCTCCACCTGGCCCTC	3062
Qy	1025	LeuLeuArgGlnLeuCysArgArgProArgSerProGlnProSerSerProAlaLeuGlu	1044
Db	3063	CTGCTCAGGCAATTGTGCAAGGGCACCCGGAGCCCCCAGCGCTCCCGGCCCTCGAG	3122
Qy	1045	HisPheArgValIleLeuSerIlysGluAlaGluIArgLysLeuLeuIhrTrpGluSerVal	1064
Db	3123	CATTCCGGGTTTACCTCTTCAAGGAAAGCCGAGGGAAAGCTCTAACGTTGGAAATCGGG	3182
Qy	1065	HisLysGluAsnPheLeuLeuAlaArgAlaArgAspLysArgGluSerAspSerGluArg	1084
Db	3183	CATAAGGAGAACCTCTGCTGGCACGGCTAGGGACAAGCGGAGAGGCGACTCCAGCGCT	3242
Qy	1085	LeuGluArgThrSerGlnLysValAspLeuAlaLeuLysGlnLeuGlyHisIleArgGlu	1104
Db	3243	CTGGAGCGCACGTCCTAGAGTTGGACTTGGCACTGGAAACAGCGGAGAGGCGACTCC	3302
Qy	1105	TyrGluGlnArgLeuLysValLeuGluArgGluValGlnGlnCysSerArgValLeuGly	1124
Db	3303	TACGAAACAGGGCCCTGAAAGTCTGGACCGGGAGGTTCCAGCAGTGTAGGCCGCTCTGGG	3362
Qy	1125	TrpValThr	1127
Db	3363	TGGGTGAGC	3371